

Resource Summary Report

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Trim Galore

RRID:SCR_011847

Type: Tool

Proper Citation

Trim Galore (RRID:SCR_011847)

Resource Information

URL: http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/

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Description: Software tool to automate quality and adapter trimming as well as quality control, with some added functionality to remove biased methylation positions for RRBS sequence files for directional, non-directional or paired-end sequencing. Wrapper around Cutadapt and FastQC to consistently apply adapter and quality trimming to FastQ files, with extra functionality for Reduced Representation Bisulfite Sequencing data.

Abbreviations: Trim Galore!

Synonyms: TrimGalore

Resource Type: software application, software resource, data processing software

Keywords: Automate, quality, adapter, trimming, remove, biased, methylation, position, RRBS, reduced, representation, bisulfite, data, sequence, wrapper, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Trim Galore

Resource ID: SCR_011847

Alternate IDs: biotools:trim_galore, OMICS_01096, SCR_016946

Alternate URLs: <https://github.com/FelixKrueger/TrimGalore>, https://bio.tools/trim_galore, <https://sources.debian.org/src/trim-galore/>

License: GNU General Public License v3.0

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Ratings and Alerts

- Used for sequencing service by the Human Islet Research Network community. Contact(s): [Golnaz Vahedi](#), [Klaus Kaestner](#) - Human Islets Research Network <https://hirnetwork.org/>

No alerts have been found for Trim Galore.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6255 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Barel M, et al. (2026) Colistin and Biofilm-Related Genes of Positive Escherichia coli O157:H7 in Cattle (Bos taurus) Carcasses Antibiotic Resistance Profiles, Biofilm and Molecular Characterisation of Isolates. Veterinary medicine and science, 12(1), e70730.

Nachtigall PG, et al. (2026) The Golden Lancehead Genome Reveals Distinct Selective Processes Acting on Venom Genes of an Island Endemic Snake. Genome biology and evolution, 18(1).

Chen Y, et al. (2026) The transcription factor CUX1 exerts opposing roles in human and mouse adipocyte differentiation. Molecular metabolism, 103, 102290.

Luo C, et al. (2026) SOX2 is a dispensable modulator of NUT carcinoma oncogenesis in mice. Life science alliance, 9(2).

Riley SE, et al. (2026) In vivo screen reveals specific roles of Hippo pathway components in development and regeneration. Life science alliance, 9(3).

Akbar H, et al. (2026) Integrated transcriptomics, proteomics, and pathway enrichment analysis in the spleen and skin of chickens reveal tissue-specific roles for the Marek's disease virus conserved herpesvirus protein kinase. Poultry science, 105(1), 106113.

Liang Y, et al. (2026) DMTF1 up-regulation rescues proliferation defect of telomere dysfunctional neural stem cells via the SWI/SNF-E2F axis. Science advances, 12(1), eady5905.

Lim KHJ, et al. (2026) Cross-presentation of dead cell-associated antigens shapes the neoantigenic landscape of tumor immunity. Nature immunology, 27(1), 72.

Kunzelman GW, et al. (2026) Chromatin Profiling Reveals Distinct Male and Female Trajectories for Developmental Learning Potential. Developmental neurobiology, 86(1), e23017.

Liu X, et al. (2026) Investigation into the Pancreatic Pathogenesis of SFTSV across Multiple Levels. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e15862.

Pena-Ortiz MA, et al. (2026) Astrocytic Chromatin Remodeler ATRX Gates Hippocampal Memory Consolidation Through Metabolic and Synaptic Regulation. *Glia*, 74(1), e70098.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Xu Y, et al. (2026) Lipid Droplet-Driven Ribosome Collisions Trigger ZAK-p38 Signaling to Accelerate Testicular Aging. *Aging cell*, 25(1), e70359.

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Basak S, et al. (2026) Novel Roles for the Ectoenzyme CD38 in the Maintenance of Transcriptional and Metabolic Homeostasis in Astrocytes. *Glia*, 74(2), e70112.

Zhang X, et al. (2026) Genetic and Functional Evidence Links Germline Biallelic Inactivating Variants in WWOX to Histological Mixed-Type Thyroid Cancer. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e07602.

Matchett CL, et al. (2026) Discovery and Validation of Molecular Biomarkers for Differentiation of Nondysplastic Barrett's Esophagus from High-grade Dysplasia and Esophageal Adenocarcinoma. *Cancer prevention research (Philadelphia, Pa.)*, 19(1), 49.

McKinney-Aguirre CA, et al. (2026) Human Placental Extract Enhances Neonatal Intestinal Epithelial Reparative Capacity in Porcine Models. *Cellular and molecular gastroenterology and hepatology*, 20(1), 101619.

Johnson NR, et al. (2026) Antagonistic regulation of nitrogen and drought signaling mediated by NIN-like protein 7 transcription factor in *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2509904122.

Zhong L, et al. (2026) Loss of FAT1 drives cyclophosphamide resistance in breast cancer via the Wnt-Catenin pathway. *International journal of biological sciences*, 22(1), 447.